

10/031331

531 Rec'd PCT/JP 18 JAN 2002

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against environmental stress and the applications

<130> 12-130

<140>

<141>

<150> JP P1999-235910

<151> 1999-07-19

<150> JP P2000-85377

<151> 2000-03-24

<160> 66

<170> PatentIn Ver. 2.1

<210> 1

<211> 1018

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (42)..(464)

<400> 1

gtccaaacag ccagagagaa acgacaacal cgaccaagaa a atg gct ctt tca agc 56

Met Ala Leu Ser Ser

1

5

tct gct ctg aga acc gtc tct tct gtg aag gtg gtc ggc cct gca 104

Ser Ala Leu Arg Thr Val Ser Ser Val Lys Val Val Gly Pro Ala

10

15

20

aga tca aag agt gct act gla ccc acc caa aca gta tlg cct ttc aag 152

Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys

25

30

35

ttc aca aac ccg tcg tta ctc act cga tcg cta agc ttt tca tca aaa 200

Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys

<211> 141
<212> PRT
<213> Bruguiera sexangula

<400> 2
Met Ala Leu Ser Ser Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys
1 5 10 15

Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr
20 25 30

Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu
35 40 45

Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
50 55 60

Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
65 70 75 80

Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
85 90 95

Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
100 105 110

Ser Leu Gly Asp Leu Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp
115 120 125

Leu Gln Lys Arg Ile Gly Val Thr Ala Glu Tyr Ala Ser
130 135 140

<210> 3
<211> 2060
<212> DNA
<213> Bruguiera sexangula

<220>
<221> CDS
<222> (81)..(1718)

<400> 3
cgaaatccct ctactaacaat taccagalcc agtctagcgt ttcgattttc tgcttcacat 60

ttctgttctt	ttgaccagaa	alg gca alc gcg gct caa act ccg gac att ctc	113
		Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu	
1		5	10
ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat	gtg gtg gca	161	
Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala			
15	20	25	
tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga	209		
Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly			
30	35	40	
ctc gac aag atg cta ggt gat gat att ggt gat gta aca att aca aat	257		
Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn			
45	50	55	
gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca	305		
Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala			
60	65	70	75
aag gtg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat	353		
Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp			
80	85	90	
gga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca	401		
Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala			
95	100	105	
aat gat ctc gtg agg aat aag alc cac cca aca tca ata atc agt gga	449		
Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly			
110	115	120	
tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg	497		
Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu			
125	130	135	
tca atg aag gtt gaa aag ctt gga aaa gat tct cta gta aac tgt gca	545		
Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala			
140	145	150	155
aag aca agc atg tcc tca aag ttg ala gct ggt gac agc gac ttc ttt	593		
Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe			
160	165	170	
gca aat ttg gtt gta gat gct gta caa gca gta aag atg acc aat gca	641		
Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala			

175	180	185	
cg g ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct			689
Arg Gly Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala			
190	195	200	
cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc			737
His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu			
205	210	215	
aat act ggt cgt gct gct caa ggg atg cct atg aga gtt gca cct gca			785
Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala			
220	225	230	235
agg att gct tgl ctt gac ttt aat cit cag aaa acg aag atg caa ttg			833
Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu			
240	245	250	
ggt gta caa gtc tta gtc act gat ccc agg gag ctt gaa aga att cgt			881
Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg			
255	260	265	
caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa			929
Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys			
270	275	280	
gct gga gca aat gtt gtt cta acc aca aag gga att gal gac atg gca			977
Ala Gly Ala Asn Val Val Thr Thr Lys Gly Ile Asp Asp Met Ala			
285	290	295	
ctt aaa tat ttt ttg gag gct ggg gct att gct ttg aga cgt gtt cg g			1025
Leu Lys Tyr Phe Val Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg			
300	305	310	315
aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt			1073
Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val			
320	325	330	
tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg			1121
Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu			
335	340	345	
ctt gga caa gct gaa gaa gtt ttg gag gag cgc att gct gat gac gat			1169
Leu Gly Gln Ala Glu Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp			
350	355	360	

gtg att alg ala aaa ggg aca aag act aca agt gcg gtt tcc ttg att		1217
Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile		
365	370	375
ctt cgt ggt gca aat gac tat atg ctc gat gag atg gag cga gcc ctt		1265
Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu		
380	385	390
395		
cat gat gct tta tgg att gtc aag aga acc ctt gaa tct aat aca gta		1313
His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val		
400	405	410
gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct ttg cac ttg gag		1361
Val Ala Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu		
415	420	425
tac ctc gct aca act ctt ggg tca cga gag cag tta gca ata gca gag		1409
Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu		
430	435	440
ttt gca gaa tcc ttg ttg att ata cca aag gtt ctt gct gtc aat gct		1457
Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala		
445	450	455
gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat		1505
Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His		
460	465	470
475		
aca gca caa aca aag gct gal aag aaa cat tta tca agc atg gga cta		1553
Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu		
480	485	490
gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att		1601
Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile		
495	500	505
510	515	520
gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca		1649
Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala		
525	530	535
540		
gag act cag aat gaa gag gaa tagatgcaga ctc ttt gtaag ctgcctccct		1748
Glu Thr Gln Asn Glu Glu Glu		

540

545

tttgttttca aattttgtgc ccttgcgcgc tggagggaaag ggggggtgtt tatgtgggt 1808
ttttagtgtt ttaatttt caaggagctc gcggccgtgt tacttttgtt tagatccat 1868
ccaaggggtg ttatggat aatgcctaag ctgtttctcg tcttttagta ggctggtagt 1928
tccactgtgt tctcaiccca attaaaagaa tggatcaaa gggccctaaa ttcgtactca 1988
ttggtgtcacg aatgttttct gacaaggata agacttgacc ctctatca caataaaaaa 2048
aaaaaaaaaa aa 2060

<210> 4

<211> 546

<212> PRT

<213> Bruguiera sexangula

<400> 4

Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu Gly Glu Arg Gln Ser
1 5 10 15

Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala Cys Gln Ala Val Ala
20 25 30

Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu
35 40 45

Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
50 55 60

Leu Lys Met Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Val Glu
65 70 75 80

Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
85 90 95

Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
100 105 110

Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
115 120 125

Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu Ser Met Lys Val Glu

130	135	140
Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser		
145	150	155
160		
Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val		
165	170	175
Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys		
180	185	190
Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala		
195	200	205
Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala		
210	215	220
Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu		
225	230	235
240		
Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu		
245	250	255
Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg Gln Arg Glu Ala Asp		
260	265	270
Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys Ala Gly Ala Asn Val		
275	280	285
Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala Leu Lys Tyr Phe Val		
290	295	300
Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg Lys Glu Asp Met Arg		
305	310	315
320		
His Val Ala Lys Ala Thr Gly Ala Thr Leu Val Ser Thr Phe Ala Asp		
325	330	335
Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu Leu Gly Gln Ala Glu		
340	345	350
Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp Val Ile Met Ile Lys		
355	360	365
Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile Leu Arg Gly Ala Asn		
370	375	380

Asp	Tyr	Met	Leu	Asp	Glu	Met	Glu	Arg	Ala	Leu	His	Asp	Ala	Leu	Cys
385				390				395				400			
Ile	Val	Lys	Arg	Thr	Leu	Glu	Ser	Asn	Thr	Val	Val	Ala	Gly	Gly	Gly
				405				410				415			
Ala	Val	Glu	Ala	Ala	Leu	Ser	Val	His	Leu	Glu	Tyr	Leu	Ala	Thr	Thr
				420				425				430			
Leu	Gly	Ser	Arg	Glu	Gln	Leu	Ala	Ile	Ala	Glu	Phe	Ala	Glu	Ser	Leu
				435				440				445			
Leu	Ile	Ile	Pro	Lys	Val	Leu	Ala	Val	Asn	Ala	Ala	Lys	Asp	Ala	Thr
				450				455				460			
Glu	Leu	Ala	Ala	Lys	Leu	Arg	Ala	Tyr	His	His	Thr	Ala	Gln	Thr	Lys
				465				470				475			480
Ala	Asp	Lys	Lys	His	Leu	Ser	Ser	Met	Gly	Leu	Asp	Leu	Ser	Lys	Gly
				485				490				495			
Thr	Ile	Arg	Asn	Asn	Leu	Glu	Ala	Gly	Val	Ile	Glu	Pro	Ala	Met	Ser
					500				505			510			
Lys	Ile	Lys	Ile	Ile	Gln	Phe	Ala	Thr	Glu	Ala	Ala	Ile	Thr	Ile	Leu
				515				520				525			
Arg	Ile	Asp	Asp	Met	Ile	Lys	Leu	Val	Lys	Asp	Glu	Thr	Gln	Asn	Glu
				530				535				540			
Glu	Glu														
	545														

<210> 5
 <211> 588
 <212> DNA
 <213> Bruguiera sexangula

<220>
 <221> CDS
 <222> (26)..(262)

<400> 5

gaaaaacaaa	gcaatcccl	gaagg	al	ct	lc	tg	g	gaa	ac	tg	g	52				
			Met	Ser	Cys	Cys	Gly	Gly	Asn	Cys	Gly					
			1				5									
tg	g	g	g	c	a	g	c	a	al	tg	g	100				
Cys	Gly	Ala	Ser	Cys	Asn	Cys	Gly	Asn	Gly	Cys	Gly	Cys				
10	15	20	25													
ta	c	c	g	a	c	at	g	g	gc	tc	g	148				
Tyr	Pro	Asp	Met	Gly	Phe	Ala	Glu	Lys	Thr	Thr	Glu	Thr				
30												Leu				
Leu	Gly	Val	Gly	Pro	Glu	Arg	Ala	His	Phe	Glu	Gly	Ala	Glu	Met	Gly	196
45												55				
tg	cc	g	cc	g	ag	aa	g	g	tc	aa	tg	g	244			
Val	Pro	Ala	Glu	Asn	Gly	Gly	Cys	Lys	Cys	Gly	Ser	Asn	Cys	Thr	Cys	
60												70				
gac	ccc	tg	c	act	tg	aaa	tg	agg	gg	aa	tg	g	292			
Asp	Pro	Cys	Thr	Cys	Lys											
75																
tat	ta	tt	at	tg	tg	tg	tg	tt	gg	tg	tt	tg	tg	352		
cg	tt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	412	
gat	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	472	
cgg	aa	tt	cc	tt	cc	tt	cc	tt	cc	tt	cc	tt	cc	tt	532	
tg	at	gg	aa	aa	gg	588										
<210>	6															
<211>	79															
<212>	PRT															
<213>	Bruguiera	sexangula														
<400>	6															
Met	Ser	Cys	Cys	Gly	Gly	Asn	Cys	Gly	Ala	Ser	Cys	Asn	Cys			
1														15		
Gly	Asn	Gly	Cys	Gly	Gly	Cys	Lys	Met	Tyr	Pro	Asp	Met	Gly	Phe	Ala	
20															30	

Glu Lys Thr Thr Glu Thr Leu Val Leu Gly Val Gly Pro Glu Arg
35 40 45

Ala His Phe Glu Gly Ala Glu Met Gly Val Pro Ala Glu Asn Gly Gly
50 55 60

Cys Lys Cys Gly Ser Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys
65 70 75

<210> 7

<211> 1280

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (1)..(1002)

<400> 7

att gaa ggg gaa gtg gtg gaa gtc caa att gat cgg ccg gcg gtg acc 48
Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp Arg Pro Ala Val Thr
1 5 10 15

ggc gcc gcg tcc aag acg ggg aaa ttg acg cta aag acg acg gag atg 96
Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met
20 25 30

gag acg gtg tac gat ttg ggg gcg aaa atg ata gag gca ttg ggg aag 144
Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys
35 40 45

gaa aag gtg cag agt ggg gat gtt att gca att gac aag gcg tcc ggc 192
Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly
50 55 60

aaa att aca aag ctt ggg cgt tca ttt tgc cgg tct agg gat tac gat 240
Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp
65 70 75 80

gcc atg gga cca cag gtg aag ttt gtt cag tgc cct gat ggg gag ctg 288
Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu
85 90 95

cag aag agg aaa gag gtc gtc cal tgl gtc tca ctc cac gag att gat	336
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp	
100 105 110	
gtt atc aat agc aga aca cag ggg ttt ctt gct ctt ttc acc ggg gat	384
Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp	
115 120 125	
act ggt gaa atc cgt gcg gag gtc agg gaa caa att gac aca aag gtc	432
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val	
130 135 140	
gct gaa tgg aga gag gaa ggg aaa gca gag att gtc cca ggt gtc ctc	480
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu	
145 150 155 160	
ttt att gat gag gtc cac atg ctt gac att gag tgc ttc tca ttt ctc	528
Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu	
165 170 175	
aat cgt gct ctt gag aat gag atg gcg cca ata tta gtt gtt gct acc	576
Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr	
180 185 190	
aac aga ggg atc acc aca atc aga ggc aca aat tac aaa tct cct cat	624
Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His	
195 200 205	
ggg att cca ata gat ctc ctt gat cga cta ctc att atc aca act caa	672
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln	
210 215 220	
cct tac aca aag gat gaa att cgt aag att ctc gat atc aga tgc cag	720
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln	
225 230 235 240	
gaa gaa gat gtc gag atg gct gaa gag gca aag gct ttc tta aca cat	768
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His	
245 250 255	
att ggg gca gaa aca tcc ttc aga tat gcc atc cat ctc att act gct	816
Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	
260 265 270	
gca gca ttc gca tgc cag aag cga aag gga aag ctt gtc gaa act gag	864
Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu	

275

280

285

gac aat agt cga gct tac aat ctg ttt ctt gat gta aag aga tct aca 912
 Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr
 290 295 300

cag tac cta ata gag tat cag aat cag tac atg ttt aat gag gca ccg 960
 Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro
 305 310 315 320

gta gga gaa ggg gac gaa gaa ggg gcc aat gcc atg ctt tct 1002
 Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser
 325 330

tgaaggccca taagctatgg agtccttgg aaacccttct ccctacttta ttgcgcac 1062
 gagccctgaa atgaagaaca atggtagact tggatccac ctggccctt atgtatgtct 1122
 tcggaaatgg aaaaaagagt ccaagaaatt tgaatttcat gaaatggag aactgaactg 1182
 tgcctactaa attgctactt tgcaagtaat gatagggcac tcacgcgtga ctggctaagt 1242
 atttatgttt ttatcatcaa aaaaaaaaaa aaaaaaaaa 1280

<210> 8

<211> 334

<212> PRT

<213> Bruguiera sexangula

<400> 8

Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp Arg Pro Ala Val Thr
 1 5 10 15

Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met
 20 25 30

Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys
 35 40 45

Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly
 50 55 60

Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp
 65 70 75 80

Ala	Met	Gly	Pro	Gln	Val	Lys	Phe	Val	Gln	Cys	Pro	Asp	Gly	Glu	Leu
85									90					95	
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp															
100								105					110		
Val	Ile	Asn	Ser	Arg	Thr	Gln	Gly	Phe	Leu	Ala	Leu	Phe	Thr	Gly	Asp
115						120						125			
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val															
130						135						140			
Ala	Glu	Trp	Arg	Glu	Glu	Gly	Lys	Ala	Glu	Ile	Val	Pro	Gly	Val	Leu
145				150					155					160	
Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu															
165						170						175			
Asn	Arg	Ala	Leu	Glu	Asn	Glu	Met	Ala	Pro	Ile	Leu	Val	Val	Ala	Thr
180						185						190			
Asn	Arg	Gly	Ile	Thr	Thr	Ile	Arg	Gly	Thr	Asn	Tyr	Lys	Ser	Pro	His
195						200						205			
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln															
210				215					220						
Pro	Tyr	Thr	Lys	Asp	Glu	Ile	Arg	Lys	Ile	Leu	Asp	Ile	Arg	Cys	Gln
225					230					235					240
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His															
245					250				255						
Ile	Gly	Ala	Glu	Thr	Ser	Leu	Arg	Tyr	Ala	Ile	His	Leu	Ile	Thr	Ala
260						265						270			
Ala	Ala	Leu	Ala	Cys	Gln	Lys	Arg	Lys	Gly	Leu	Val	Glu	Thr	Glu	
275						280						285			
Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr															
290				295					300						
Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro															
305				310					315					320	
Val	Gly	Glu	Gly	Asp	Glu	Glu	Gly	Ala	Asn	Ala	Met	Leu	Ser		

<210> 9

<211> 420

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (27)..(194)

<400> 9

cgaaagatata aagtgatcggt cgagcg atg ggt cac tct aac gtc tgg aac tct 53

Met Gly His Ser Asn Val Trp Asn Ser

1 5

cac ccc aag aac tac ggc cct ggt tcc cgc gcc tgg ggt ggg 101
His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly
10 15 20 25aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag 149
Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln
30 35 40tgc ttc cgt agc aat gcc aag gaa att ggc ttc att aag tac cgc 194
Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg
45 50 55

tgaatgtatat cgataatggcc cagaatggcc tggggcggtt cgtgttcgtat ttcgtatgtt 254

cccccttttc ggttgtttttt taggacaatg ttcgtttttt tttatgtttt gttttttttt 314

gactgtatgtt gaactaacga tttttttttt gttttttttt tttttttttt 374

gtatcatcatc cttttttttt tttttttttt aaaaaaaaaaaa aaaaaaa 420

<210> 10

<211> 56

<212> PRT

<213> Bruguiera sexangula

<400> 10

Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Asn Tyr Gly Pro

1	5	10	15
Gly Ser Arg Ala Cys Arg Val Cys Gly Asn Pro His Gly Leu Ile Arg			
20		25	
30			
Lys Tyr Gly Leu Met Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys			
35		40	
45			
Glu Ile Gly Phe Ile Lys Tyr Arg			
50		55	

acg gtc att gat gct cct gga cat cgt gac ttt att aag aat atg atc	342
Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile	
90 95 100	
acc ggg act tcc caa gct gac tgc gct gtc ctc atc att gac tct acc	390
Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr	
105 110 115	
act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag	438
Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu	
120 125 130 135	
cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc	486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys	
140 145 150	
tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat	534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr	
155 160 165	
gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac	582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Val Gly Tyr	
170 175 180	
aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac	630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp	
185 190 195	
aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act	678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr	
200 205 210 215	
ctt ctt gag gcc ctg gac atg alc cag gag cca aag agg cca tca gat	726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp	
220 225 230	
aag ccc ctc cgt ctc cca ctt cag gal gtg tac aag att ggt ggt att	774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile	
235 240 245	
ggg aca gtc cca gtg ggt cgt gtt gaa act ggt gtc ctg aag cct gga	822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly	
250 255 260	
atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct	870

Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser				
265	270	275		
gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac				918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn				
280	285	290	295	
gtt ggc ttc aat gtt aag aat gtt tcc gtg aag gat ctt aag cgg ggt				966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly				
300	305	310		
tat gtt gcc tca aac tcc aag gal gat cct gcc aag gag gca tct agc				1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser				
315	320	325		
ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat				1062
Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile Gly Asn				
330	335	340		
ggt tat gcc cct gtt ctg gat tgc cac acc tct cac att gct gtc aag				1110
Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala Val Lys				
345	350	355		
ttt tct gag atc ctc aca aag att gat agg cga tct ggc aag gag ctt				1158
Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys Glu Leu				
360	365	370	375	
gaa aag gag ccc aag ttc tlg aag aat ggt gat gct ggg ttc gtg aag				1206
Glut Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Phe Val Lys				
380	385	390		
atg att ccg acc aag cct atg gtg gtg gaa act ttc tcc gag tat cct				1254
Met Ile Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu Tyr Pro				
395	400	405		
ccg ctt ggt aga ttt gcc glc agg gac atg cgc cag act gtt gca gtg				1302
Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val				
410	415	420		
gga gtc atc aag agt glc gag aaa aag gaa cct tct gga gct aag gtg				1350
Gly Val Ile Lys Ser Val Glu Lys Lys Glu Pro Ser Gly Ala Lys Val				
425	430	435		
act aaa tct gct gcc aag aag ggt ggc aaa tgaaccgtgc aagtcaagat				1400
Thr Lys Ser Ala Ala Lys Lys Gly Gly Lys				
440	445			

tga~~tg~~tgat gaaggctatt ggaagaataa agactggcc ctggtagcg gtc~~ta~~at 1460
 tggatgtca gcagttggtt tcgagaacta cagttcaat tcagcgccat calcacggag 1520
 ctgttgtcc cagaattggg ttc~~t~~gaccg tcgg~~tg~~gat tggc~~t~~gg tttgagtgac 1580
 ttc~~t~~ttgtcatgtt~~ta~~ga ctta~~t~~cgga tttgctatt cataaagcgg ctggaa~~t~~ 1640
 taaaaaaaaaa aaaaaaaaaaa aaaa 1664

<210> 12

<211> 449

<212> PRT

<213> Bruguiera sexangula

<400> 12

Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val
 1 5 10 15

Asp Ser Gly Lys Ser Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
 20 25 30

Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
 35 40 45

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
 50 55 60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
 65 70 75 80

Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
 85 90 95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
 100 105 110

Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
 115 120 125

Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly
 130 135 140

Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Ser

145	150	155	160
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ser			
165	170	175	
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Glu Lys Ile Pro Phe Val Pro			
180	185	190	
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu			
195	200	205	
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Met Ile Gln			
210	215	220	
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp			
225	230	235	240
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu			
245	250	255	
Thr Gly Val Leu Lys Pro Gly Met Val Val Thr Phe Gly Pro Ser Gly			
260	265	270	
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ala Leu Gln			
275	280	285	
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser			
290	295	300	
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp			
305	310	315	320
Pro Ala Lys Glu Ala Ser Ser Phe Thr Ser Gln Val Ile Ile Met Asn			
325	330	335	
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His			
340	345	350	
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp			
355	360	365	
Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn			
370	375	380	
Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val			
385	390	395	400

Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
405 410 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys
420 425 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly
435 440 445

Lys

<210> 13

<211> 770

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (2)..(769)

<400> 13

c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49
Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
1 5 10 15

agc gtg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97
Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
20 25 30

agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145
Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
35 40 45

tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193
Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
50 55 60

gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc 241
Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
65 70 75 80

aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289

Lys	Met	Ile	Arg	Tyr	Pro	Leu	Glu	Val	Leu	Ala	Ile	Phe	Asp	Ile	Val	
																85
																90
																95
ttg atg gat att glg agt ttg atc aac cct ttg ttt gag aaa cat gta															337	
Leu	Met	Asp	Ile	Val	Ser	Leu	Ile	Asn	Pro	Leu	Phe	Glu	Lys	His	Val	
																100
																105
																110
caa gtc agg att ttc aat ctt aag acc tgc att aca atg aga aat ctc															385	
Gln	Val	Arg	Ile	Phe	Asn	Leu	Lys	Thr	Ser	Ile	Thr	Met	Arg	Asn	Leu	
																115
																120
																125
aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ata att															433	
Asn	Pro	Ser	Asp	Ile	Glu	Lys	Met	Val	Ser	Leu	Lys	Gly	Met	Ile	Ile	
																130
																135
																140
cgg tgt agt tcc ata ata ccg gag atc agg gaa gca gta ttt aga tgc															481	
Arg	Cys	Ser	Ser	Ile	Ile	Pro	Glu	Ile	Arg	Glu	Ala	Val	Phe	Arg	Cys	
																145
																150
																155
																160
ctt gtt tgl ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg															529	
Leu	Val	Cys	Gly	Tyr	Phe	Ser	Asp	Pro	Ile	Val	Val	Asp	Arg	Gly	Arg	
																165
																170
																175
ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac															577	
Ile	Ser	Glu	Pro	Lys	Ala	Cys	Leu	Lys	Glu	Glu	Cys	Leu	Thr	Lys	Asn	
																180
																185
																190
tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att															625	
Ser	Met	Thr	Leu	Val	His	Asn	Arg	Cys	Arg	Phe	Ala	Asp	Lys	Gln	Ile	
																195
																200
																205
gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca															673	
Val	Arg	Leu	Gln	Glu	Thr	Pro	Asp	Glu	Ile	Pro	Glu	Gly	Gly	Thr	Pro	
																210
																215
																220
cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag															721	
His	Thr	Val	Ser	Leu	Leu	Met	His	Asp	Lys	Leu	Val	Asp	Ala	Gly	Lys	
																225
																230
																235
																240
cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a															770	
Pro	Gly	Asp	Arg	Val	Glu	Val	Thr	Gly	Ile	Tyr	Arg	Ala	Met	Ser	Val	
																245
																250
																255

<210> 14
<211> 256

<212> PRT

<213> Bruguiera sexangula

<400> 14

Asp	Asp	Met	Asp	Glu	Ala	Thr	Pro	Thr	Phe	Val	Trp	Gly	Thr	Asn	Ile
1				5				10						15	
Ser	Val	Gln	Asp	Val	Lys	Ala	Ala	Ile	Gln	Met	Phe	Leu	Lys	His	Phe
				20				25					30		
Arg	Asp	Ser	Asn	Gln	Ser	Gln	Arg	Asn	Glu	Ile	Phe	Glu	Glu	Gly	Lys
				35				40					45		
Tyr	Val	Lys	Ala	Ile	His	Lys	Val	Leu	Glu	Val	Glu	Gly	Glu	Ser	Leu
				50				55				60			
Asp	Val	Asp	Ala	Arg	Asp	Val	Phe	Asp	Tyr	Asp	Ser	Asp	Leu	Tyr	Ala
				65			70				75		80		
Lys	Met	Ile	Arg	Tyr	Pro	Leu	Glu	Val	Leu	Ala	Ile	Phe	Asp	Ile	Val
				85				90					95		
Leu	Met	Asp	Ile	Val	Ser	Leu	Ile	Asn	Pro	Leu	Phe	Glu	Lys	His	Val
				100				105					110		
Gln	Val	Arg	Ile	Phe	Asn	Leu	Lys	Thr	Ser	Ile	Thr	Met	Arg	Asn	Leu
				115				120				125			
Asn	Pro	Ser	Asp	Ile	Glu	Lys	Met	Val	Ser	Leu	Lys	Gly	Met	Ile	Ile
				130				135				140			
Arg	Cys	Ser	Ser	Ile	Ile	Pro	Glu	Ile	Arg	Glu	Ala	Val	Phe	Arg	Cys
				145			150				155		160		
Leu	Val	Cys	Gly	Tyr	Phe	Ser	Asp	Pro	Ile	Val	Val	Asp	Arg	Gly	Arg
				165				170				175			
Ile	Ser	Glu	Pro	Lys	Ala	Cys	Leu	Lys	Glu	Glu	Cys	Leu	Thr	Lys	Asn
				180				185				190			
Ser	Met	Thr	Leu	Val	His	Asn	Arg	Cys	Arg	Phe	Ala	Asp	Lys	Gln	Ile
				195			200				205				
Val	Arg	Leu	Gln	Glu	Thr	Pro	Asp	Glu	Ile	Pro	Glu	Gly	Gly	Thr	Pro
				210			215				220				

His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys
225 230 235 240

Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val
245 250 255

<210> 15

<211> 846

<212> DNA

<213> *Mesembryanthemum crystallinum*

<220>

<221> CDS

<222> (39)..(530)

<400> 15

caaattttct tlgctgaatc gaatctacaa. aatacctg atg ggt cag gtt ctt gac 56
Met Gly Gln Val Leu Asp
1 5

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca 104
Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr
10 15 20

gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt 152
Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu
25 30 35

aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata 200
Thr Phe Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile
40 45 50

aac aag tat ttt ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa 248
Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys
55 60 65 70

atc aga gcc ttt atg cag gaa tgc gat atg gat gtc gal gga gaa ctt 296
Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu
75 80 85

aac cgt gag gaa ttt gtc aag ttc atg cag aag gtc aca gcc gat aca 344
Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr
90 95 100

ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca	392		
Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro			
105	110	115	
aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg	440		
Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val			
120	125	130	
ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg	488		
Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val			
135	140	145	150
acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc	530		
Thr Leu Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys			
155	160		
tgatttagagg cttagtttac ttgtttca taca tacagaagga acagttttgg tcaatttttt 590			
tcttttttaa taggacataa ggaagtgtt tttttttttt ccagggtttt 650			
gggaaatgg gaaagaacat acaaatgtt tcaactgcgt attggctgtat ccctccat 710			
ataaaaactt gtcgtgttca gcatgagcga ttcaatattt gcaatgtca atatttgtaa 770			
tgttgttac attcagttgtat tagtttttttgcgcatttttggaaaaaaa aaaaaaaaaa 830			
aaaaaaaaaaa aaaaaaa	846		

<210> 16

<211> 164

<212> PRT

<213> *Mesembryanthemum crystallinum*

<400> 16

Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys

1 5 10 15

Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro

20 25 30

Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu

35 40 45

Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp

50 55 60

```

<210> 17
<211> 872
<212> DNA
<213> Mesembryanthemum crystallinum

<220>
<221> CDS
<222> (183)..(569)

<400> 17
aacaaaatgt ctctctcttt ctctttctct ttctctttct ctctcttcgt gggltgtatgt 60
agtaagcctt gtccttttgc tctctgttga atgtactatc ttctgtgttgaac caaaggccaa 120
agatataacta ttggagattt ctctactcgtaa aatttgtttt taggtgttga ccctgtttag 180
ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att 227
  Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile
    1           5           10          15
gct att atc gcg gat gag gal act gta aci gga ttt ttg clg gct gga 275
  Ala Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly

```

20	25	30														
gtt ggt aat gtt gat cta cga aga cag aca aat tac att att ggt gac 323																
Val	Gly	Asn	Val	Asp	Leu	Arg	Arg	Gln	Thr	Asn	Tyr	Ile	Ile	Val	Asp	
35			40			45										
aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca 371																
Asn	Lys	Thr	Thr	Met	Lys	Gln	Ile	Glu	Asp	Ala	Phe	Lys	Glu	Phe	Thr	
50			55			60										
gca aga gag gac att gct gtt gta cta atc agc caa tat gtt gca aat 419																
Ala	Arg	Glu	Asp	Ile	Ala	Val	Val	Leu	Ile	Ser	Gln	Tyr	Val	Ala	Asn	
65			70			75										
atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att 467																
Met	Ile	Arg	Val	Leu	Val	Asp	Ser	Tyr	Asn	Lys	Pro	Ile	Pro	Ala	Ile	
80			85			90			95							
ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca 515																
Leu	Glu	Ile	Pro	Ser	Lys	Asp	His	Pro	Tyr	Asp	Pro	Asn	His	Asp	Ser	
100			105			110										
gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc 563																
Val	Leu	Ser	Arg	Val	Lys	Tyr	Leu	Phe	Ser	Ser	Glu	Ser	Ala	Ser	Ser	
115			120			125										
aga ttt tagccatcg ctttggaaag ttccttcgtc ctgtttttt ggtttttttt 619																
Arg	Phe															
atgtttttt acttggatgtt agttttttttt gttttttttt gttttttttt 679																
ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt
ttttttttttt aaggatgtt attacgtttt cttttttttt gttttttttt gttttttttt 739																
ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt
atgtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 799																
ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt
ttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 859																
ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt	ttttttttttt
aaaaaaaaaaa aaa 872																

<210> 18

<211> 129

<212> PRT

<213> *Mesembryanthemum crystallinum*

<400> 18

Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala			
1	5	10	15
Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val			
20	25	30	
Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn			
35	40	45	
Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala			
50	55	60	
Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met			
65	70	75	80
Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu			
85	90	95	
Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val			
100	105	110	
Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg			
115	120	125	
Phe			

<210> 19
<211> 647
<212> DNA
<213> *Mesembryanthemum crystallinum*

<220>
<221> CDS
<222> (64) . . (426)

Gln	Glu	Gln	Ile	His	Ile	Lys	Ile	Arg	Ile	Thr	Leu	Ser	Ser	Lys	Asn	Val
20															30	
aag	aac	ctt	gag	aaa	gtg	tgt	gct	gal	ctt	gta	cgc	ggt	gca	aag	gac	204
Lys	Asn	Leu	Glu	Lys	Val	Cys	Ala	Asp	Leu	Val	Arg	Gly	Ala	Lys	Asp	
35														45		
aag	cgc	ctc	agg	gtt	aag	gga	cca	gtg	agg	atg	ccc	acc	aag	gtt	ctg	252
Lys	Arg	Leu	Arg	Val	Lys	Gly	Pro	Val	Arg	Met	Pro	Thr	Lys	Val	Leu	
50													60			
aag	atc	aca	aca	agg	aag	tct	ccc	tgt	ggt	gaa	gga	acc	aac	acc	ttt	300
Lys	Ile	Thr	Thr	Arg	Lys	Ser	Pro	Cys	Gly	Glu	Gly	Thr	Asn	Thr	Phe	
65													75			
gac	aga	ttt	gag	ttg	cgt	gtt	cac	aag	aga	gtc	att	gac	ctc	ttc	agc	348
Asp	Arg	Phe	Glu	Leu	Arg	Val	His	Lys	Arg	Val	Ile	Asp	Leu	Phe	Ser	
80												90		95		
tcc	cca	gac	gtg	gtc	aag	cag	atc	acc	tcc	atc	acc	att	gaa	cct	ggt	396
Ser	Pro	Asp	Val	Val	Lys	Gln	Ile	Thr	Ser	Ile	Thr	Ile	Glu	Pro	Gly	
100												105		110		
gtt	gag	gtt	gag	gtt	aca	ata	gct	gac	tct	tagacatgcc	tgttgaagt					446
Val	Glu	Val	Glu	Val	Thr	Ile	Ala	Asp	Ser							
115												120				
gtcgtcgttg	tagggctgtt	giagcigtc	cataatgg	tgctatc	ctaagaat	ttt										506
tgaagatact	aaatgttttg	ttt	gaaagag	aigtttctt	tagctgtaat	gttatgttt										566
tgaagggttt	ggaacatgca	ttat	tgtta	aigctttatc	aatagaactt	ccaa	ttt	gaa								626
tgc	aaaaaaa	aaaaaaa	aaaaaaa	a												647

<210> 20

<211> 121

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 20

Met	Ala	Tyr	Ala	Met	Lys	Pro	Thr	Lys	Pro	Gly	Met	Glu	Glu	Ser	Gln
1					5						10			15	

Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys

20	25	30
Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys		
35	40	45
Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys		
50	55	60
Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp		
65	70	75
Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser		
85	90	95
Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val		
100	105	110
Glu Val Glu Val Thr Ile Ala Asp Ser		
115	120	

<210> 21
 <211> 686
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (62)..(493)

<400> 21
 acaccattca caaaacacat taaaaaaaaa cactacttct ttctttctta gccacttggaa 60

a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109
 Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
 1 5 10 15

ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157
 Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
 20 25 30

caa tct gtg gag gag tct aag gga tac ggi ggt ggg cac gga ggt cac 205
 Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly His Gly Gly His
 35 40 45

35

40

45

Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly
50 55 60

His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro
65 70 75 80

Gln Gly Gly Tyr Gly His Gly His Gly Gly Tyr Gly His Gly Gly
85 90 95

Gly Tyr Gly His Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His
100 105 110

Gly Gly Gly Tyr Gly His Gly Gly Tyr Gly His Gly Gly His Gly
115 120 125

Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn
130 135 140

<210> 23

<211> 683

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (48)..(362)

<400> 23

gttaagatat tatattgcaa ctttacaaag catttctgca actaaat atg gcc ttt 56
Met Ala Phe
|

tcc aaa cct cta att gct tct cta ctt ctt tct ctc ttt gtt ctt cag 104
Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe Val Leu Gln
5 10 15

ttt gtt cat gca gtt gaa cct att tca tcc tcc aat caa gtg ggt agc 152
Phe Val His Ala Val Glu Pro Ile Ser Ser Asn Gln Val Gly Ser
20 25 30 35

aac act gga ggt acc tca gag agt aaa gtg gat tgt ggg gcg gca tgt 200
Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly Ala Ala Cys

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro
65 70 75 80

Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr
85 90 95

Thr His Gly Asn Arg His Lys Cys Pro
100 105

<210> 25

<211> 803

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (51)..(593)

<400> 25

cgcgacgcgt tcagctcttt ctctctcttt ctctctccctc accgtggaaag atg ggg 56
Met Gly
1

ttg tca ttt acc aaa tlg ttt agc cgg tig ttc gct aag aag gaa atg 104
Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met
5 10 15

cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc 152
Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu
20 25 30

tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga 200
Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly
35 40 45 50

ttt aat gtg gag act gta gaa tac aag aac atc agc ttc act gtg tgg 248
Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp
55 60 65

gat gtc ggg ggt caa gac aag att cgt cca tlg tgg aga cat tac ttc 296
Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe
70 75 80

Ile	Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile	Pro	Thr
35							40						45		
Ile	Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Ser	Phe	Thr
50							55					60			
Val	Trp	Asp	Val	Gly	Gly	Gln	Asp	Lys	Ile	Arg	Pro	Leu	Trp	Arg	His
65						70			75				80		
Tyr	Phe	Gln	Asn	Thr	Gln	Gly	Leu	Ile	Phe	Val	Val	Asp	Ser	Asn	Asp
85								90				95			
Arg	Asp	Arg	Val	Val	Glu	Ala	Arg	Asp	Glu	Leu	His	Arg	Met	Leu	Asn
100							105					110			
Glu	Asp	Glu	Leu	Arg	Asp	Ala	Val	Leu	Leu	Val	Phe	Ala	Asn	Gln	
115							120					125			
Asp	Leu	Pro	Asn	Ala	Met	Asn	Ala	Ala	Glu	Ile	Thr	Asp	Lys	Leu	Gly
130							135					140			
Leu	His	Ser	Leu	Arg	Gln	Arg	His	Trp	Tyr	Ile	Gln	Ser	Thr	Cys	Ala
145							150					155			160
Thr	Ser	Gly	Glu	Gly	Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Asn	Asn
165								170					175		
Ile	Ala	Ser	Lys	Ala											
180															

<210> 27
 <211> 680
 <212> DNA
 <213> Avicennia marina

<220>
 <221> CDS
 <222> (161)..(454)

<400> 27
 ctaaaagcca aaggcaagat aagaaacagg ttccttttagc tatcttcctc gtcgtcgctgc 60
 tgcaaaagt tccatccccag aagaatcagga aaacccttctc gcagcagcac tctaataatc 120

ctccaatltt	gatcaagag	aagaaacaaa	alaaacagaa	atg	gct	cgc	tct	ttc	175							
				Met	Ala	Arg	Ser	Phe								
				1				5								
tcc	aac	gct	aag	acc	gtc	tct	gtc	att	gcc	aac	atc	tca	gtc	223		
Ser	Asn	Ala	Lys	Thr	Val	Ser	Ala	Val	Ile	Ala	Asn	Glu	Ile	Ser	Ala	
				10				15				20				
ctt	gtc	acc	agg	agg	gtt	tat	gtc	gtc	ctc	gca	cag	ggc	gtt	gtt	tcg	271
Leu	Val	Thr	Arg	Arg	Gly	Tyr	Ala	Ala	Leu	Ala	Gln	Gly	Val	Val	Ser	
				25				30				35				
agc	agc	gct	aga	agc	ggc	gct	ccg	aac	glg	atg	cgt	aag	aaa	gga	319	
Ser	Ser	Ala	Arg	Ser	Gly	Gly	Ala	Pro	Asn	Val	Met	Leu	Lys	Lys	Gly	
				40				45				50				
tcc	gaa	gaa	tcc	ggg	aag	aca	gca	tgg	glg	ccc	gac	ccg	gac	acc	ggc	367
Ser	Glu	Glu	Ser	Gly	Thr	Ala	Trp	Val	Pro	Asp	Pro	Asp	Thr	Gly		
				55			60				65					
tac	tac	cga	ccg	gga	aac	gag	gac	aag	gcc	gct	cgt	gac	ccg	gtc	gag	415
Tyr	Tyr	Arg	Pro	Gly	Asn	Glu	Asp	Lys	Ala	Ala	Leu	Asp	Pro	Val	Glu	
				70			75				80				85	
cgt	cgg	gag	atg	clc	atc	aag	aac	aag	ccc	agc	cga	caa	tgaatgaacc		464	
Leu	Arg	Glu	Met	Leu	Ile	Lys	Asn	Lys	Pro	Ser	Arg	Gln				
				90			95									
aagaatgtg	ggatccat	taatccccc	ccgttctgg	tccatcgatc	gaatctgaa	524										
cgttgcgtc	tctagaaatt	cgtccatcg	gaaatctatc	aaagtctgtt	tcttgcatt	584										
ggcgtttcc	gtccatata	tgtatgtcc	caggtgtggc	ctgggggtgg	ttagatgata	644										
tataaaatgt	ggtaatata	aaaaaaa	aaaaaa			680										

<210> 28
 <211> 98
 <212> PRT
 <213> Avicennia marina

<400> 28
 Met Ala Arg Ser Phe Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala
 1 5 10 15

Asn Glu Ile Ser Ala Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala
20 25 30

Gln Gly Val Val Ser Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val
35 40 45

Met Leu Lys Lys Gly Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro
50 55 60

Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala
65 70 75 80

Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser
85 90 95

Arg Gln

<210> 29

<211> 490

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (20)..(349)

<400> 29

tggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52
Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile
1 5 10

gct agc cgc aac aga tct ttc gtc atc gca tct cca aag gaa gat gag 100
Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu
15 20 25

aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148
Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly
30 35 40

gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctc 196
Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu
45 50 55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca	244		
Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr			
60	65	70	75
gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc	292		
Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile			
80	85	90	
gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac	340		
Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr			
95	100	105	
aaa tcg gct taagatgtg tglagacaa tggtcgacg tggaaatgt	389		
Lys Ser Ala			
110			
tgccatgact tggtttatg tggatttcaa gtttctgaaa ctagcatttt gattttgtt	449		
tccaaatgcaa tggcattat gggaaaaaaa aaaaaaaaaa a	490		
<210> 30			
<211> 110			
<212> PRT			
<213> Avicennia marina			
<400> 30			
Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg			
1	5	10	15
Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser			
20	25	30	
Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala			
35	40	45	
Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr			
50	55	60	
Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile			
65	70	75	80
Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr			
85	90	95	

Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala
100 105 110

<210> 31
<211> 592
<212> DNA
<213> *Avicennia marina*

<220>
<221> CDS
<222> (75)...(320)

〈400〉 31

```

aagattcagc caag atg cag aac gaa gag ggg caa aac atg gal cic tac 110
          Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr
          1           5           10

```

atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158
 Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp
 15 20 25

cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206
His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg
30 35 40

tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct	254
Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala	
45 50 55 60	

cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa 302
 Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys
 65 70 75

glc gaa acc agg cag cag tgalcccgct caaltcagca gtgaaaglt 350
Val Glu Thr Arg Gln Gln
80

tttgggtttt gttctggtt gtgttatata tgctttcca gaatcaattt cttgtacttgga 410

ttggatgtttt aaaaatggat gctaaagggtt gggagacccgg atgcctttgt tactcgatgt 470

atcacaaggta galactgggc ttaglaatgc gtagataatgg tgccttgctc ttagccatgg 530

gactacgaat cagttatgig attagacaat gtaatcicc aaaaaaaaaa aaaaaaaaaa 590
aa 592

<210> 32
<211> 82
<212> PRT
<213> Avicennia marina

<400> 32
Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys
1 5 10 15
Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val
20 25 30
Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln
35 40 45
Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala
50 55 60
Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg
65 70 75 80
Gln Gln

<210> 33
<211> 1806
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (362)..(1552)

<400> 33
tggaaaggta aagtttacag ctttttcgc gcccgtcggt tgattacgttggat 60
ttggaaatgtt gatagcgctgt agttagccgtt gcccgtggat ggtaatgttgc attttaggaa 120

tacgggttttgcgc agttttactgt tccttaggtt tggcccttgc ggcttcttggg 180
 attgggatt taatcgctga tcgaacagtt tccggagaa aataciccta gtgcgcata 240
 atctgattttgcgacgagaa attgatacac ggttttgcgtt tttgcgcatt 300
 agatacicccg agtgctcgct agatgtggat aatccggagg gctgtttcgat tgagatgagg 360
 g atg tta tca ggg tta atg aac ttc ctg tgg gcc ttt cgg cca agg 409
 Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
 1 5 10 15
 gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat 457
 Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
 20 25 30
 ggg ctt tta tgg tat aag gac ttt ggg caa cat atc aat gga gag ttt 505
 Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
 35 40 45
 tca atg gct gta gtt caa gca aat aac tta cta gag gat cag agt caa 553
 Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
 50 55 60
 ctt gaa tct ggt tgc ctg agc ttt agt gat tca gga caa tat ggc act 601
 Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
 65 70 75 80
 ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt 649
 Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
 85 90 95
 atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat 697
 Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
 100 105 110
 caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa 745
 Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
 115 120 125
 gaa ggt ttt ttc tgc gtt gtt agc aga caa tgg tcc atg caa cca cag 793
 Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
 130 135 140
 att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgc agt ggc 841
 Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly

145	150	155	160	
act ctt tat gtt tcc aac ctt ggt gal tcc cgt gct gtt ctt ggg acg				889
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr				
165	170	175		
ctt tcc aag gct aca ggg gaa gta cag gct act caa ctc tca aca gag				937
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu				
180	185	190		
cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac				985
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His				
195	200	205		
cca gat gac tca cag att gtg gtt cta aag cat aat gta tgg cga gtg				1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val				
210	215	220		
aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa				1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys				
225	230	235	240	
aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt				1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg				
245	250	255		
gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg				1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val				
260	265	270		
cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc				1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly				
275	280	285		
ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa				1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys				
290	295	300		
cat cca cac aat ggg att gct aga aga tta gta aaa gca gct ttg caa				1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln				
305	310	315	320	
gag gca gca aag aaa agg gaa alg agg tac tcg gat ttg aag aaa att				1369
Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile				
325	330	335		

gac	cgt	ggg	gtt	cgc	cgt	cat	gtc	cat	gac	atc	act	gtt	gtg	gtg	1417	
Asp	Arg	Gly	Val	Arg	Arg	His	Phe	His	Asp	Asp	Ile	Thr	Val	Val	Val	
340							345						350			
gtg	ttt	ctt	gac	tca	cac	ctt	gtg	agc	cg	gct	agc	tca	gtc	cg	ggc	1465
Val	Phe	Leu	Asp	Ser	His	Leu	Val	Ser	Arg	Ala	Ser	Ser	Val	Arg	Gly	
355							360						365			
cca	aac	atc	tcc	gtg	aaa	ggt	ggc	ggc	atc	agt	ctg	cct	ccc	aat	gct	1513
Pro	Asn	Ile	Ser	Val	Lys	Gly	Gly	Gly	Ile	Ser	Leu	Pro	Pro	Asn	Ala	
370							375						380			
ctt	gca	cct	tgt	gcc	aca	cca	acg	gag	cca	gtc	cca	aat	tgtatgtct			1562
Leu	Ala	Pro	Cys	Ala	Thr	Pro	Thr	Glu	Pro	Val	Pro	Asn				
385						390							395			
gtctcttta	atgttatttc	ccgttagcc	tgttgtacta	tgttatgtg	aatacaggta											1622
gtt	ttaac	ggataacagc	ggcccttggaa	tcttttaatc	catactgtaa	c	t	t	t	aaccg						1682
gagacttta	cttggcatag	tttcaatgcc	caagggatac	atagacgtgg	acaagccatc											1742
tttggcggtga	caatcatcat	agttttagttt	tctggcata	tctttcaaaa	aaaaaaaaaa											1802
aaaaa																1806

<210> 34
 <211> 397
 <212> PRT
 <213> Avicennia marina

<400> 34																
Met	Leu	Ser	Gly	Leu	Met	Asn	Phe	Leu	Trp	Ala	Cys	Phe	Arg	Pro	Arg	
1					5					10				15		
Ala	Asp	Arg	Ser	Val	His	Thr	Gly	Ser	Asp	Ala	Gly	Gly	Arg	Gln	Asp	
					20				25				30			
Gly	Leu	Leu	Trp	Tyr	Lys	Asp	Leu	Gly	Gln	His	Ile	Asn	Gly	Glu	Phe	
					35				40				45			
Ser	Met	Ala	Val	Val	Gln	Ala	Asn	Asn	Leu	Leu	Glu	Asp	Gln	Ser	Gln	
					50				55				60			
Leu	Glu	Ser	Gly	Cys	Leu	Ser	Leu	Ser	Asp	Ser	Gly	Gln	Tyr	Gly	Thr	

65	70	75	80
Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe			
85	90	95	
Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His			
100	105	110	
Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu			
115	120	125	
Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln			
130	135	140	
Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly			
145	150	155	160
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr			
165	170	175	
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu			
180	185	190	
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His			
195	200	205	
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val			
210	215	220	
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys			
225	230	235	240
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg			
245	250	255	
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val			
260	265	270	
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly			
275	280	285	
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys			
290	295	300	
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln			
305	310	315	320

Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile
325 330 335

Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val
340 345 350

Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly
355 360 365

Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala
370 375 380

Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn
385 390 395

<210> 35

<211> 743

<212> DNA

<213> *Mesembryanthemum crystallinum*

<220>

<221> CDS

<222> (1)..(420)

<400> 35

cct gag cta gca cct aaa gat ggg gat ttc cgt ttc aat atc tct gag 48
Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
1 5 10 15

cct gaa gct atg cta cca gct gga act gta gat cat gct gtt gaa agg 96
Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
20 25 30

att tat caa gag atg ccg cgg tgg gaa gag act gtt tta ggt tcc agg 144
Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
35 40 45

agc aga tat gag cat gtc att cag gca ctt gca gat aaa tac cct tca 192
Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
50 55 60

gaa aat ttg ttg cta gtt acg cat ggt gaa ggt gtt ggg act tca gtt 240
Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val

<210> 36
<211> 140
<212> PRT
<213> *Mesembryanthemum crystallinum*

<400> 36
 Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
 1 5 10 15
 Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
 20 25 30
 Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
 35 40 45

Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
50 55 60

Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
65 70 75 80

Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
85 90 95

Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
100 105 110

Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
115 120 125

Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
130 135 140

<210> 37

<211> 348

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)..(246)

<400> 37

atc att gct ccc cta gct att ggt ttt atc gtt ggt gcc aac atc tta 48
Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
1 5 10 15

gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96
Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
20 25 30.

ggc ccc gcc gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144
Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
35 40 45

gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192
Ala Gly Pro Leu Ile Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
50 55 60

atc ttt att ggt cac caa gag cca gct tcc gct gac tac cag aga ctc 240
Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
65 70 75 80

tct gct taagaatii aatctttgc cctaggaaa aatgtttat gcatgtatii 296
Ser Ala

tgtattttg ttgggtctaa aatttatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38

<211> 82

<212> PRT

<213> Sueada japonica

<400> 38

Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
1 5 10 15

Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
20 25 30

Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
35 40 45

Ala Gly Pro Leu Ile Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
50 55 60

Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
65 70 75 80

Ser Ala

<210> 39

<211> 1602

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)..(1419)

<400> 39

cac acc gtt gal tta acc att gaa gct atg atg ctc gat tct caa gct	48
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala	
1 5 10 15	
tct gal ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg	96
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro	
20 25 30	
cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt	144
Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg	
35 40 45	
ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctt gat	192
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp	
50 55 60	
ttc att gag agt gct atc aag aag aat gaa gta atc aat ggg cac tac	240
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr	
65 70 75 80	
aaa aat gtc aag ttt atg ttt gct gat gtg act tct ccc act ctc agt	288
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser	
85 90 95	
ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg	336
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met	
100 105 110	
tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa	384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys	
115 120 125	
tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct ttt cat	432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His	
130 135 140	
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa	480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu	
145 150 155 160	
cct agg ttc tac act aag gcc ttc aaa gag ttt cat ttg caa gat gga	528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly	
165 170 175	
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa ttt att gga	576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly	

180	185	190	
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg tgg tgg			624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp			
195	200	205	
caa aaa gtt gat tct aag gat gal aag ggg ttc cag cga ttt ctg gat			672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp			
210	215	220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt			720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe			
225	230	235	240
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt			768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe			
245	250	255	
gtg tca atg ctg gac ttt aag cct ggc cag aag gtc ctg gat gtt ggt			816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly			
260	265	270	
tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt			864
Cys Gly Ile Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val			
275	280	285	
gag gtt gtt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt			912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu			
290	295	300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat			960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp			
305	310	315	320
tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc			1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser			
325	330	335	
cgt gac acc att ctg cat att cag gac aag cct gcg ttt ttt aga tcc			1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser			
340	345	350	
tcc tac aaa tgg ttt aag cca gga ggt aaa gtt cta atc agt gat tac			1104
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr			
355	360	365	

tgc aag aaa gct ggl cca ccc tca cct gaa ttc gcc gct tac aat aag	1152		
Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys			
370	375	380	
cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt	1200		
Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu			
385	390	395	400
aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag	1248		
Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln			
405	410	415	
ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag	1296		
Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys			
420	425	430	
gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt	1344		
Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val			
435	440	445	
gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga	1392		
Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg			
450	455	460	
tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac	1439		
Trp Gly Leu Phe Val Ala Lys Lys Lys			
465	470		
tggcactgtc gat ttc tag tattatctt caatgtttt aigtaatgtt ctctatcatg	1499		
taaaatggcc aataagggtc atttcgcaga ctgtaaatgtt attaaatcata ttttatctt	1559		
taattatca tggattttatg caaaaaaaaaaaa aaaaaaaaaaaa aaa	1602		
<210> 40			
<211> 473			
<212> PRT			
<213> Sucada japonica			
<400> 40			
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala			
1	5	10	15
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro			
20	25	30	

Pro	Leu	Glu	Gly	Lys	Cys	Leu	Leu	Glu	Leu	Gly	Ala	Gly	Ile	Gly	Arg
						35			40					45	
Phe	Thr	Gly	Glu	Leu	Ala	Glu	Lys	Ala	Gly	Gln	Val	Ile	Ala	Leu	Asp
						50			55				60		
Phe	Ile	Glu	Ser	Ala	Ile	Lys	Lys	Asn	Glu	Val	Ile	Asn	Gly	His	Tyr
						65			70			75			80
Lys	Asn	Val	Lys	Phe	Met	Cys	Ala	Asp	Val	Thr	Ser	Pro	Thr	Leu	Ser
						85			90				95		
Phe	Pro	Pro	His	Ser	Leu	Asp	Val	Ile	Phe	Ser	Asn	Trp	Leu	Leu	Met
						100			105				110		
Tyr	Leu	Ser	Asp	Glu	Glu	Val	Glu	Asn	Leu	Val	Glu	Arg	Met	Leu	Lys
						115			120				125		
Trp	Leu	Lys	Pro	Gly	Gly	Tyr	Ile	Phe	Phe	Arg	Glu	Ser	Cys	Phe	His
						130			135				140		
Gln	Ser	Gly	Asp	His	Lys	Arg	Lys	Ser	Asn	Pro	Thr	His	Tyr	Arg	Glu
						145			150			155			160
Pro	Arg	Phe	Tyr	Thr	Lys	Ala	Phe	Lys	Glu	Cys	His	Leu	Gln	Asp	Gly
						165			170				175		
Ser	Gly	Asn	Ser	Tyr	Glu	Leu	Ser	Leu	Leu	Ser	Cys	Lys	Cys	Ile	Gly
						180			185				190		
Ala	Tyr	Val	Arg	Asn	Lys	Lys	Asn	Gln	Asn	Gln	Ile	Ser	Trp	Leu	Trp
						195			200				205		
Gln	Lys	Val	Asp	Ser	Lys	Asp	Asp	Lys	Gly	Phe	Gln	Arg	Phe	Leu	Asp
						210			215				220		
Thr	Ser	Gln	Tyr	Lys	Cys	Asn	Ser	Ile	Leu	Arg	Tyr	Glu	Arg	Val	Phe
						225			230			235			240
Gly	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Gly	Tyr	Glu	Thr	Thr	Lys	Glu	Phe
						245			250				255		
Val	Ser	Met	Leu	Asp	Leu	Lys	Pro	Gly	Gln	Lys	Val	Leu	Asp	Val	Gly
						260			265				270		

Cys	Gly	Ile	Gly	Gly	Gly	Asp	Phe	Tyr	Met	Ala	Glu	Thr	Phe	Asp	Val
275						280					285				
Glu	Val	Val	Gly	Phe	Asp	Leu	Ser	Val	Asn	Met	Ile	Ser	Phe	Ala	Leu
290						295					300				
Glu	Arg	Ser	Ile	Gly	Leu	Lys	Cys	Ala	Val	Glu	Phe	Glu	Val	Ala	Asp
305						310				315					320
Cys	Thr	Lys	Ile	Asn	Tyr	Pro	Asp	Asn	Ser	Phe	Asp	Val	Ile	Tyr	Ser
325						330					335				
Arg	Asp	Thr	Ile	Leu	His	Ile	Gln	Asp	Lys	Pro	Ala	Leu	Phe	Arg	Ser
340						345					350				
Phe	Tyr	Lys	Trp	Leu	Lys	Pro	Gly	Gly	Lys	Val	Leu	Ile	Ser	Asp	Tyr
355						360					365				
Cys	Lys	Lys	Ala	Gly	Pro	Pro	Ser	Pro	Glu	Phe	Ala	Ala	Tyr	Ile	Lys
370						375					380				
Gln	Arg	Gly	Tyr	Asp	Leu	His	Asp	Val	Lys	Glu	Tyr	Gly	Gln	Met	Leu
385						390				395					400
Lys	Asp	Ala	Gly	Phe	Val	Asp	Val	Leu	Ala	Glu	Asp	Arg	Thr	Glu	Gln
405						410					415				
Phe	Ile	Arg	Val	Leu	Arg	Lys	Glu	Leu	Glu	Thr	Val	Glu	Lys	Glu	Lys
420						425					430				
Asp	Val	Phe	Ile	Ser	Asp	Phe	Ser	Glu	Glu	Asp	Tyr	Asn	Asp	Ile	Val
435						440					445				
Gly	Gly	Trp	Asn	Asp	Lys	Leu	Arg	Arg	Thr	Ala	Lys	Gly	Glu	Gln	Arg
450						455					460				
Trp	Gly	Leu	Phe	Val	Ala	Lys	Lys	Lys							
465						470									

<210> 41
 <211> 1251
 <212> DNA
 <213> Salsola komarovii

<220>
<221> CDS
<222> (1)..(933)

<400> 41

cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gta caa ggt 48
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
1 5 10 15

gag gtc att gaa caa tct ttt gga gag gag cac ttt ttt aga aca 96
Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
20 25 30

tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca 144
Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
35 40 45

atc tct cct aaa cca gaa tgg cgt gca ctt ttt gac gag atg gct gtt 192
Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
50 55 60

gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt 240
Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65 70 75 80

gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg 288
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
85 90 95

aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa 336
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Ile Glu
100 105 110

act ctg cgt gca att cct tgg ata ttt tcg tgg aca caa acc agg ttt 384
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
115 120 125

cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt 432
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
130 135 140

gac aag gac att aag aat ctt tcg ata ctc aag gcc atg tat aat gag 480
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145 150 155 160

tgg ccg ttc ttc aga gtt act att gal ctc tta gaa aat gtt ttc act 528

gagttatatt gagtagttt tcttttta aaaaaaaaaa aaaaaaaaa

1251

<210> 42

<211> 311

<212> PRT

<213> *Salsola komarovii*

<400> 42

Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
1 5 10 15

Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
20 25 30

Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
35 40 45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
50 55 60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65 70 75 80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
85 90 95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Ile Glu
100 105 110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
115 120 125

His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
130 135 140

Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145 150 155 160

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
165 170 175

Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
180 185 190

Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp
195 200 205

Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu
210 215 220

Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile
225 230 235 240

Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp
245 250 255

Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
260 265 270

Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
275 280 285

Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
290 295 300

Ala Gly Met Gln Asn Thr Gly
305 310

<210> 43

<211> 637

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (1)..(339)

<400> 43

caa tac ttg gta aat gaa gtg aag aaa act gtt cag ggg cgt gct caa 48
Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
1 5 10 15

ctt ggt gtg gaa gca ttt gct gat gcg ctt ctt gtg gtt cca aag acg 96
Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
20 25 30

ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt 144
Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu

35

40

45

acg gga gaa tat gaa aaa ggg aat g₁g g₁a g₁a c₁t a₁a c₁t a₁c a₁c a₁a 192
 Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
 50 55 60

gga gaa cct ata gat cct caa alg gag ggt atc ttt gac aat tat tcc 240
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
65 70 75 80

ctt ctt gtc gag gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg 336
 Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
 100 105 110

aat tagtttcac cctagttttt gtagttttgg taaatgtttt 389
Asn

aggtagggtc akggttcctt ttttttagcc taaggcactat gtttttttttttggcc 449

tttgaatlll galcatcagg cggttgaact tttgccttgtl tacaatttgc accagaaatt 509

tacacttgt gcttagcaaa gaatggaaa aaaaggaatt gatttatca aaaaaaaaaa 629

〈210〉 44

〈211〉 113

<212> PRT

<213> *Avicennia marina*

〈400〉 44

Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
1 5 10 15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
 20 25 30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu
35 40 45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
50 55 60

Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
65 70 75 80

Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu
85 90 95

Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
100 105 110

Asn

<210> 45

<211> 741

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (3)..(293)

<400> 45

aa gag atc aat tgc ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47
Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser
1 5 10 15

cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95
Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn
20 25 30

tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143
Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys
35 40 45

gca aaa gat cga ctg cct cgt cgg acg gtc aag ata gat ata aac atc 191
Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile
50 55 60

gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239
Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile

85

90

95

Leu

<210> 47

<211> 983

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (1)..(762)

<400> 47

atg	tgc	ctt	cat	cac	cac	ttt	tca	tct	tca	tct	tct	tct	ttt	ctt	ctt	48
Met	Phe	Leu	His	His	His	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Leu	Leu	
1			5				10						15			

ctc	ttc	tcc	tct	ctc	ctt	ctt	tca	tct	gct	aat	ctt	tat	cat	96		
Leu	Phe	Phe	Ser	Leu	Leu	Ile	Phe	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	His	
20				25							30					

cag	aat	caa	gga	tct	tgt	agt	gac	ttt	gaa	tca	gaa	cca	tca	aig	gct	144
Gln	Asn	Gln	Gly	Ser	Cys	Ser	Asp	Phe	Glu	Ser	Glu	Pro	Ser	Met	Ala	
35			40								45					

act	ctt	ggt	gga	ttg	cgc	gaa	tcc	cat	ggt	gct	tct	aat	gat	gct	gag	192
Thr	Leu	Gly	Gly	Leu	Arg	Glu	Ser	His	Gly	Ala	Ser	Asn	Asp	Ala	Glu	
50			55							60						

att	gaa	acc	ctt	gct	cgc	ttt	gct	gtt	gat	gaa	cac	aac	aaa	aaa	gag	240
Ile	Glu	Thr	Leu	Ala	Arg	Phe	Ala	Val	Asp	Glu	His	Asn	Lys	Lys	Glu	
65			70							75		80				

aat	gca	ttg	ttg	gag	ttt	gca	agg	gtt	gtt	aag	gca	aag	gaa	cag	gtg	288
Asn	Ala	Leu	Leu	Glu	Ala	Arg	Val	Val	Val	Lys	Ala	Lys	Glu	Gln	Val	
85			90							95						

gtt	gct	ggc	ggt	aca	ttg	cat	cac	tgc	act	atc	gaa	gca	att	gaa	gct	336
Val	Ala	Gly	Thr	Leu	His	His	Phe	Thr	Ile	Glu	Ala	Ile	Glu	Ala	Gly	
100				105						110						

aag	aag	aag	cic	tac	gaa	gct	aag	gtg	ttg	gtg	aag	cca	ttg	aig	aac	384
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<210> 48
<211> 254

<212> PRT

<213> Salsola komarovii

<400> 48

Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Phe Leu Leu
1 5 10 15

Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His
20 25 30

Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala
35 40 45

Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
50 55 60

Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu
65 70 75 80

Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
85 90 95

Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
100 105 110

Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
115 120 125

Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
130 135 140

Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
145 150 155 160

Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
165 170 175

Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
180 185 190

Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
195 200 205

Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
210 215 220

Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
225 230 235 240

Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
245 250

<210> 49

<211> 543

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (3)..(389)

<400> 49

aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc 47
Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val
1 5 10 15

gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt 95
Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly
20 25 30

agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttt 143
Ser Gly Gly Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu
35 40 45

ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191
Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu
50 55 60

aag cat ctc aaa gtt aag gcc aag aat gtg gtt gag atg ccc gga 239
Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly
65 70 75

aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttt gcc cga aaa 287
Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys
80 85 90 95

gat ttc ggg tat aaa ccc aci acc gal ttt caa acc ggg ttt aaa aag 335
Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys
100 105 110

```

III gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct 383
Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro
115 120 125

```

gta aat taatataaa atataagtaa tattttttt ctctttttt ataaattaca 439
Val Asn

gaattatttttttggggggttttatgaattttttggataatatggggattttttttc 499

taaaatgggaa aaataagaat ccaaggaaaa aaaaaaaaaa aaaa 543

<210> 50

〈211〉 129

〈212〉 PRT

〈213〉 *Salsola komarovii*

<400> 50

Asn	Lys	Val	Asp	Leu	Ala	Arg	Asp	Phe	Thr	Phe	Ile	Asp	Asp	Val	Val
1				5					10					15	

Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser
20 25 30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly
35 40 45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys
50 55 60

His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn
65 70 75 80

Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp
85 90 95

Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe
 100 105 110

Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val
115 120 125

Asn

<210> 51
<211> 1219
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (2).. (871)

<400> 51

c aca gga gca aac aaa gga aia gga ctt gaa cta tgc aaa caa cta gct 49
Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
1 5 10 15

gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97
Ala Lys Gly Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
20 25 30

tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat 145
Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
35 40 45

ctt cac ttt cat cag ctc gal gtt act gac atc act agt att gct gct 193
Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
50 55 60

att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg 241
Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
65 70 75 80

aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata 289
Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
85 90 95

gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt 337
Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
100 105 110

ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa 385
Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
115 120 125

aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttt ccg ctt 433
Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
130 135 140

ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta 481
 Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
 145 150 155 160

 gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga 529
 Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
 165 170 175

 gat gcc gag agc ctt aca gaa gaa cga ata gal gag att ctg aat gac 577
 Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
 180 185 190

 atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct 625
 Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
 195 200 205

 aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac 673
 Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
 210 215 220

 aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att 721
 Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
 225 230 235 240

 tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg 769
 Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
 245 250 255

 ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc 817
 Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
 260 265 270

 caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg 865
 Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
 275 280 285

 ttt gaa taaaacaatt tgcctttaa aaccaacacc acatatctttaa gaattttcca 921
 Phe Glu
 290

 ttgttaggca tctttacgaa aaaaataaga cactgtcaat actgtttactg gaaaatgcaa 981
 tgcactttttt tcatgtatgc atggcgcagg tttttatctt gactgtcaaca ataaagatctt 1041

 gtttttcaaa ggcactttaa ggaatgttga tgcacccgttcaaaacaaggc agacaagatgtt 1101

<210> 52
<211> 290
<212> PRT
<213> Sueada japonica

〈400〉 52

Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
1 5 10 15

Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
20 25 30

Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
35 40 45

Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
50 55 60

Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
65 70 75 80

Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
85 90 95

Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
100 105 110

Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
115 120 125

Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
 130 135 140

Leu Lys Leu Scr Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
145 150 155 160

Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
165 170 175

Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp

180	185	190
Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro		
195	200	205
Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr		
210	215	220
Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile		
225	230	235
Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu		
245	250	255
Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro		
260	265	270
Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser		
275	280	285
Phe Glu		
290		

<210> 53
 <211> 1148
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (3)..(848)

<400> 53

ga	agg	ccg	gat	alc	cat	gtt	gaa	caa	gct	cat	tca	gat	gat	att	47
Ser	Arg	Pro	Asp	Ile	His	Val	Glu	Gln	Ala	His	Ser	Asp	Asp	Ile	
1			5						10			15			

act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctc ttt tct aga agt 95
 Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser
 20 25 30

ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct 143
 Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser
 35 40 45

ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc	191		
Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val			
50	55	60	
tca ttt agt cca gat gag cag ctc atc ttt act ggt aca tct gta gaa	239		
Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu			
65	70	75	
agg gat agc cca act gga gga ttt ttt tgc ttt tat gat cgg gaa aaa	287		
Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys			
80	85	90	95
ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg	335		
Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val			
100	105	110	
caa ttt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga	383		
Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly			
115	120	125	
aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt	431		
Asn Lys Ser Gln Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser			
130	135	140	
gag aga ggt gct ctt glg tgg gtt gct cgt gca cca agg atg aaa tca	479		
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser			
145	150	155	
gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt	527		
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu			
160	165	170	175
ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att	575		
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile			
180	185	190	
ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga	623		
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly			
195	200	205	
cct ggc cat ggt ggc aga act ggt aca tca tgg ggt agt ttt tta aca	671		
Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr			
210	215	220	
caa tat ctc ctc aag caa ggg ggc atg ttt aaa gag aca tgg atg gat	719		

Gln	Tyr	Leu	Leu	Lys	Gln	Gly	Gly	Met	Leu	Lys	Glu	Thr	Trp	Met	Asp	
225					230				235							
gaa	gat	ccc	aga	gaa	gct	att	cic	aag	tat	gct	gat	gct	gca	gaa	aag	767
Glu	Asp	Pro	Arg	Glu	Ala	Ile	Leu	Lys	Tyr	Ala	Asp	Ala	Ala	Glu	Lys	
240				245				250				255				
gat	cca	aag	ttt	att	gcc	ccg	gct	tat	gct	gag	act	cag	ccc	aag	cca	815
Asp	Pro	Lys	Phe	Ile	Ala	Pro	Ala	Tyr	Ala	Glu	Thr	Gln	Pro	Lys	Pro	
				260				265			270					
gtc	ttt	gag	gtt	ttt	gat	tct	gat	aag	gaa	gat	gaa	gaa	taatttcatctt	tttgcaggg	868	
Val	Phe	Glu	Asp	Ser	Asp	Lys	Glu	Asp	Glu	Glu						
		275			280											
ttggatttaat	tttaattttag	aatattatac	tgtgtatatt	aatagccat	ttttcaggcg											928
aatgataatgc	tttctcacatt	acatgctgag	ttttatttgc	tgctacagat	tgttagatgaa											988
taggttaatg	taaacacaag	catagagatt	agaatataga	aatgattctg	tatccaaaac											1048
acaatttat	caccagaatgg	tatcaaagc	tgtattgact	gtttagtataat	gtcatttaacc											1108
acttttac	cccaaaaaaa	aaaaaaaaaa	aaaaaaaaaa													1148
<210> 54																
<211> 282																
<212> PRT																
<213> Sueada japonica																
<400> 54																
Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr																
1		5		10		15										
Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe																
	20			25		30										
Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu																
	35			40		45										
Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser																
	50			55		60										
Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg																
	65			70		75			80							

Asp Ser Pro Thr Gly	Gly Leu Leu Cys	Phe Tyr Asp Arg Glu Lys Leu	
85		90	95
Glu Leu Val Ser Lys Val Gly	Ile Ser Pro Thr Cys Ser Val Val Gln		
100	105		110
Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly Asn			
115	120		125
Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser Glu			
130	135		140
Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser Val			
145	150	155	160
Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu Pro			
165	170		175
Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile Leu			
180	185		190
Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly Pro			
195	200	205	
Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr Gln			
210	215	220	
Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp Glu			
225	230	235	240
Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys Asp			
245	250		255
Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro Val			
260	265	270	
Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu			
275	280		

<210> 55
 <211> 1193
 <212> DNA
 <213> Avicennia marina

<220>
<221> CDS
<222> (3)..(815)

<400> 55

gt gca cct gag tta ctt ctt gga gca aag cat tat aca agt gct gtt 47
Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val
1 5 10 15

gac atg tgg gct gtg ggc tgc att ttt gct gag ctt ctg act cta aag 95
Asp Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys
20 25 30

cca cta ttt caa ggg caa gaa gta aaa ggg act tct aat cca ttt cag 143
Pro Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln
35 40 45

ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa 191
Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln
50 55 60

gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg 239
Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val
65 70 75

caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt lac aat gtt 287
Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val
80 85 90 95

gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg 335
Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Ser Lys Met
100 105 110

ctt gag tat gat cct aga aaa aga ata aca aca gct aca caa gct ctt gag 383
Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu
115 120 125

cat gag tat ttt cgc atg gaa cct ttt ccg gga cgc aac gct ctg gta 431
His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val
130 135 140

cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg 479
Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val
145 150 155

<210> 56
<211> 271
<212> PRT

<213> Avicennia marina

<400> 56

Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp
1 5 10 15

Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro
20 25 30

Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu
35 40 45

Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu
50 55 60

Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln
65 70 75 80

Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val
85 90 95

His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu
100 105 110

Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His
115 120 125

Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro
130 135 140

Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp
145 150 155 160

Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro
165 170 175

Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val
180 185 190

Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln
195 200 205

Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala
210 215 220

Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val

225 230 235 240

Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro Gly
245 250 255

Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
260 265 270

<210> 57
<211> 1195
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (116)..(1195)

<400> 57
gcaaaagtaa gaglgaaaaga acacaaacca actttctatt tttagctcaa atcaaattca 60

atagtgccaa aacaatagag ggcaaattct cattgccccaa ttcaaatttg gtaaa atg 118
Met
1

gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gal caa gaa ccc ttt 166
Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe
5 10 15

cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214
His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys
20 25 30

caa gaa tta gta gta ccc aaa tca aaa ctt caa ctc aaa aag cca aag 262
Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys
35 40 45

cca aaa cca att tca aaa age act tca gtt ttg tgc aaa aat gct tgc 310
Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys
50 55 60 65

ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta 358
Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu
70 75 80

ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta	406		
Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val			
85	90	95	
ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct	454		
Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala Ala			
100	105	110	
att cga att caa acc cac aaa tct aaa ccc aaa acc cag att aaa aat	502		
Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys Asn			
115	120	125	
tcg ggt ttt ggg cta ttc ggg tca atg tta aag cga tta aat ctt cga	550		
Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu Arg			
130	135	140	145
aat cgt acc caa aaa atc aag tca aaa aca gag gaa caa aac aga gga	598		
Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg Gly			
150	155	160	
tgc tct gtt ttg agg agt gtt gaa gaa gaa aaa act acc acc att tct	646		
Cys Ser Val Leu Arg Ser Val Glu Glu Lys Thr Thr Thr Ile Ser			
165	170	175	
tct tct tca tct tca tct tca aca tca tcg tat tct tcg tgt tct	694		
Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys Ser			
180	185	190	
tgc aat gag agg tta agt agt ttg gat ttg gag agt tct agc agt gga	742		
Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser Gly			
195	200	205	
aga tca tta cat gat gaa gat gaa gat gaa gat gat gaa ttt	790		
Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Asp Glu Phe			
210	215	220	225
gag ttt aca aat gtt tta aga gaa aat aat aat gat gat aaa aat gga	838		
Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn Gly			
230	235	240	
ggt tat tat tca gga att tgc tta agt cct ttg agt cca ttt cgt ttt	886		
Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg Phe			
245	250	255	
gct ctt cat aaa aac tct tct cct gaa cgt tgc tct cct gct aaa tcc	934		
Ala Leu His Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys Ser			

260	265	270	
cct gtt cgt tgc aaa ttt gag ggt aat gct aaa tat gaa caa gaa agc			982
Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu Ser			
275	280	285	
tta ata aag ttt gaa gac gaa gat gaa gaa gac aaa gag caa aat agc			1030
Leu Ile Lys Phe Glu Asp Glu Asp Glu Asp Lys Glu Gln Asn Ser			
290	295	300	305
cct gtt tcc gtg ctc gat cct cca ttc gag gat gat tac gat ggg cat			1078
Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly His			
310	315	320	
gag gag gat agc tac gag gac alc gaa tgc agc tat gct ttt gta caa			1126
Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val Gln			
325	330	335	
aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cta			1174
Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu			
340	345	350	
gcg gag ttg gac cca att gaa			1195
Ala Glu Leu Asp Pro Ile Glu			
355	360		
<210> 58			
<211> 360			
<212> PRT			
<213> Sueada japonica			
<400> 58			
Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro			
1	5	10	15
Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys			
20	25	30	
Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro			
35	40	45	
Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala			
50	55	60	
Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys			

65	70	75	80
Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg			
85	90	95	
Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala			
100	105	110	
Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys			
115	120	125	
Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu			
130	135	140	
Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg			
145	150	155	160
Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile			
165	170	175	
Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys			
180	185	190	
Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser			
195	200	205	
Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu			
210	215	220	
Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn			
225	230	235	240
Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg			
245	250	255	
Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys			
260	265	270	
Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu			
275	280	285	
Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Asp Lys Glu Gln Asn			
290	295	300	
Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly			
305	310	315	320

His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val
325 330 335

Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys
340 345 350

Leu Ala Glu Leu Asp Pro Ile Glu
355 360

<210> 59

<211> 1301

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (3)..(815)

<400> 59

gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac 47
Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn
1 5 10 15

ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa 95
Leu Ser Ile Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln
20 25 30

gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt 143
Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu
35 40 45

ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa 191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu
50 55 60

acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca 239
Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro
65 70 75

gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt 287
Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val
80 85 90 95

ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt	335		
Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe			
100	105	110	
gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata	383		
Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile			
115	120	125	
cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa	431		
Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu			
130	135	140	
gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga	479		
Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg			
145	150	155	
atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg	527		
Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met			
160	165	170	175
aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg	575		
Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser			
180	185	190	
gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt	623		
Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val			
195	200	205	
gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat	671		
Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn			
210	215	220	
gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg	719		
Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val			
225	230	235	
ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga	767		
Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg			
240	245	250	255
att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc	815		
Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu			
260	265	270	
taactttcta ttatccatcc tgggatttgg glacgaaagt ctgccttcaa gatgcgtaa	875		

caigtlglgl attacaacig tgigaalcia glaagtttgtl agggtgagat tgltccgtal 935
 ctatlgcac agccggtlgg gagagatlgc tgcicaaca acgtacaaaa tlggggcalg 995
 ttaacggata glalgcagtl gtaattttgtl acatcacatt tggatgtt agtcaglaca 1055
 tcataactag ctcctccat acttcctcaaa tggcaactg gaatagatgtt ttagatata 1115
 tagatcttc tttgtatggaa aatgtttcag ggtacaacaagc cagaaatcaa aatggttta 1175
 tggtaaaaaa tataacttia aatgttttgtl aggaagtttc tggatggttt tggatggct 1235
 ttaacaact acatcgatia aggaatccg tatacacaat tcaacaatgaa aaaaaaaaaa 1295
 aaaaaaa 1301

<210> 60
 <211> 271
 <212> PRT
 <213> Salsola komarovii

<400> 60
 Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn Leu
 1 5 10 15
 Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln Glu
 20 25 30
 Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu Phe
 35 40 45
 Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu Thr
 50 55 60
 Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp
 65 70 75 80
 Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val Leu
 85 90 95
 Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe Glu
 100 105 110
 Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro
 115 120 125

Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu
 130 135 140
 Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile
 145 150 155 160
 Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys
 165 170 175
 Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp
 180 185 190
 Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu
 195 200 205
 Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val
 210 215 220
 Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu
 225 230 235 240
 Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile
 245 250 255
 Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu
 260 265 270

<210> 61
 <211> 1032
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (1)..(732)

<400> 61
 cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt 48
 Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
 1 5 10 15
 caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg 96
 Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro

20	25	30	
gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc			144
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu			
35	40	45	
tcg cgc tac tcc ccc gtg atc ggc ctc ggc gtc caa tgg aag ccc tcc			192
Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser			
50	55	60	
tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc			240
Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu			
65	70	75	80
atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac			288
Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp			
85	90	95	
ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac ggc cgt			336
Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg			
100	105	110	
gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat			384
Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn			
115	120	125	
ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac tgg aag tgg tcc			432
Leu Val Asp Leu Ala Glu Glu Asn Gly His Tyr Leu Lys Trp Ser			
130	135	140	
atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgg ggg gta cac aaa			480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys			
145	150	155	160
ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat			528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn			
165	170	175	
gac cag gtt cag tat gct tgg gat gct tac gtt tct ctt cgt ctt			576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu			
180	185	190	
gct cga gct tat ggg tac cac cgt ctc gat cac gal gal gat tat gat			624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp			
195	200	205	

gac	cat	gac	gac	gal	gal	aac	gac	cac	acc	gal	gal	gal	lac	gal	gac	672
Asp	His	Asp	Asp	Asp	Asp	Asn	Asp	Asp	His	Thr	Asp	Asp	Asp	Tyr	Asp	Asp
210															220	
gtt	tac	gac	cgc	aat	ata	ggc	tct	gal	gal	gal	ggt	tat	gal	gcc	gal	720
Val	Tyr	Asp	Arg	Asn	Ile	Gly	Ser	Asp	Asp	Asp	Gly	Tyr	Asp	Ala	Asp	
225															240	
gat	gal	cga	cga	tgtcaat	ttt	ggactagact	tgc	tat	ttgg	aagggtccga						772
Asp	Asp	Arg	Arg													
tcatca	gcc	agtc	taat	ta	caa	agagaca	aga	aaata	aaa	atgtat	ca	aaaaa	aga	ag		832
tcaatccata																
tat	tcgt	taat	ttt	tca	atgc	aat	ttt	tg	ttt	ta	ttt	ggc	tt	ttt	ggc	892
gtataat	atag	ttt	ttt	taat	atgc	act	at	at	at	at	ttt	ttt	ttt	ttt	ttt	
gc	tat	gcgc	tgtat	gtcc	ata	acca	at	ttt	ttt	tca	ttt	ttt	ttt	ttt	ttt	952
caaaaaaaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	1032

<210> 62
 <211> 244
 <212> PRT
 <213> Salsola komarovii

Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe																
1				5					10					15		
Gln	His	Arg	Asn	Pro	His	His	Arg	Asp	Leu	His	Pro	Cys	Arg	Ser	Pro	
															20	
															25	
															30	
Ala	Met	Gly	Pro	Leu	Pro	Pro	Gln	Thr	His	Leu	Arg	Trp	Tyr	Ser	Leu	
															35	
															40	
															45	
Ser	Arg	Tyr	Ser	Pro	Val	Ile	Gly	Leu	Gly	Val	Gln	Trp	Lys	Pro	Ser	
															50	
															55	
															60	
Ser	Thr	Ser	Ala	Ala	Thr	Leu	Gln	Leu	Ser	Ile	Asp	Lys	Lys	Cys	Leu	
															65	
															70	
															75	
Ile	Phc	Gln	Leu	Ser	His	Ser	Pro	Ala	Ile	Pro	Ala	Thr	Leu	Arg	Asp	
															85	
															90	
															95	

Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
 100 105 110
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn
 115 120 125
 Leu Val Asp Leu Ala Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
 130 135 140
 Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
 145 150 155 160
 Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
 165 170 175
 Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
 180 185 190
 Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
 195 200 205
 Asp His Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
 210 215 220
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
 225 230 235 240
 Asp Asp Arg Arg

<210> 63
 <211> 1029
 <212> DNA
 <213> *Mesembryanthemum crystallinum*

<220>
 <221> CDS
 <222> (3)..(824)

<400> 63
 ca cat atc agc cac atc cac tta att ccc cac agt ctt agt ctg tta 47
 His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu
 1 5 10 15

gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca	95		
Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser			
20	25	30	
cct tct gcc ctt cta tcc acc tcc aca tcc acc tca aca acc cct ctt	143		
Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Thr Pro Leu			
35	40	45	
aaa gct ccc ccc ttg gcc tta acc aag acc cac gta acg atc cca tca	191		
Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser			
50	55	60	
tca tca aag cca ccc cta acc aat tta act acc agt tta act gct gtc	239		
Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val			
65	70	75	
gcc aca gct gct gcc ata aic ctg tcc aca acc cct cca tcg ttt gct	287		
Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala			
80	85	90	95
gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca	335		
Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala			
100	105	110	
agt gca gcc aat tat gga ggc tac ggt ggc aat tcg aac aag aaa gat	383		
Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Asn Ser Asn Lys Lys Asp			
115	120	125	
tca gct gag tac ata tat gac gtc cct gca ggt tgg aaa gag aga cta	431		
Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu			
130	135	140	
gta tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc	479		
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe			
145	150	155	
aac ccc aag aag aca gag cga gag tac ctt acc tac ctt gct ggt	527		
Asn Pro Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly			
160	165	170	175
att agg caa cta ggt ccc aaa gaa gtt atc ctc aac aac tta gca ctc	575		
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu			
180	185	190	
tca gat gtg aac ctg caa gat caa att tcc agt gca gac tct gtg aca	623		
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr			

195	200	205	
tca gaa gag agg aaa gat gac aag gga cag gtt tac tat gat tat gag			671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu			
210	215	220	
att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg			719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg			
225	230	235	
aac aag cta tat gct cat ttt gtt agc gca cca aca ccc gaa tgg aat			767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn			
240	245	250	255
cgg gat caa gat atg ctg agg cac alc cac aac tca ttt aca aca gtc			815
Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val			
260	265	270	
ggg tca ttc tagaaaggt atatgataat cattataga gatgtcagag			864
Gly Ser Phe			
aggcatacat ttgaatgtac ttctgtgag ctggacttct tgaatctgt aacatgtaa			924
cgaaaattct ttctgggtta tcagaaacct agtgagtgct tggaaacttgc aatgagaaac			984
tctcaataa acaatgtac ttgtatcaaaaa aaaaaaaaaa aaaaa			1029
<210> 64			
<211> 274			
<212> PRT			
<213> <i>Mesembryanthemum crystallinum</i>			
<400> 64			
His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp			
1	5	10	15
Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro			
20	25	30	
Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Pro Leu Lys			
35	40	45	
Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser			
50	55	60	

Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala
65 70 75 80

Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp
85 90 95

Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser
100 105 110

Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser
115 120 125

Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val
130 135 140

Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn
145 150 155 160

Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile
165 170 175

Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser
180 185 190

Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser
195 200 205

Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile
210 215 220

Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn
225 230 235 240

Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn Arg
245 250 255

Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val Gly
260 265 270

Ser Phe

<210> 65
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 65
gcctcgagaa ccgtctagac tttagatgaag gtg

33

<210> 66
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 66
tcctcgttc atctcgagct attacagct

30